

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WASTFALT, Maria K. Boden
FLOCK, Jan-Ingmar
- (ii) TITLE OF INVENTION: FIBRINOGEN BINDING PROTEIN
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
(B) STREET: P.O. Box 1404
(C) CITY: Alexandria
(D) STATE: Virginia
(E) COUNTRY: United States
(F) ZIP: 22313-1404
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: TBA (Div of US 09/276,141)
(B) FILING DATE: Even date herewith
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/276,141
(B) FILING DATE: 25-03-99
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/244,229
(B) FILING DATE: 09-DEC-1994
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: SE 9202720-0
(B) FILING DATE: 21-SEP-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: SE 9302955-1
(B) FILING DATE: 13-SEP-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/SE93/00759
(B) FILING DATE: 20-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: McGowan, Malcolm K.

2025 SEP 17 09:20

(B) REGISTRATION NUMBER: 39,300
(C) REFERENCE/DOCKET NUMBER: 012889-011

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (703) 836-6620
(B) TELEFAX: (703) 836-2021

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Asn Ser
1 5 10 15

Lys Tyr Gly Thr
 20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Val Thr Lys Asp Tyr Ser Lys Glu Ser Arg Val Asn Glu Lys Ser
1 5 10 15

Lys Lys Gly Ala
 20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser
 1 5 10 15
 Lys Asn Gly Thr
 20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ile Val Thr Lys Asp Tyr Ser Gly Lys Ser Gln Val Asn Ala Gly Ser
 1 5 10 15
 Lys Asn Gly Thr
 20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His
1 5 10 15

Asn Ile Val Glu
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Tyr Pro Glu Lys Lys Pro Val
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGCGAAGGA TACGGTCCAA GAGAAAAGAA ACCAGTGAGT ATTAATCACA ATATCGTAGA	60
GTACAATGAT GGTACTTTTA AATATCAATC TAGACCAAAA TTAACTCAA CACCTAAATA	120
TATTAAATTC AAACATGACT ATAATATTTT AGAATTTAAC GATGGTACAT TCGAATATGG	180
TGCACGTCCA CAATTTAATA AACCAGCAGC GAAAAGTATG GCAACTATTA AAAAGAACA	240
AAAATTGATT CAAGCTCAA ATCTGTGAG AGAATTTGAA AAAACACATA CTGTCAGTGC	300
ACACAGAAAA GCACAAAAGG CAGTCAACTT AGTTTCGTTT GAATACAAAG TGAAGAAAAT	360
GGTCTTACAA GAGCGAATTG ATAATGTATT AAAACAAGGA TTAGTGAG	408

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His	
1 5 10 15	
Asn Ile Val Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro	
20 25 30	
Lys Phe Asn Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn	
35 40 45	

Val Leu Lys Gln Gly Leu Val Arg
130 135

ATT GCG TCA ACA GCA GAT GCG AGC GAA GGA TAC GGT CCA AGA GAA AAG
Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro Arg Glu Lys
25 30 35

AAA Lys	CCA Pro	GTG Val	AGT Ser	ATT Ile	AAT Asn	CAC His	AAT Asn	ATC Ile	GTA Val	GAG Glu	TAC Thr	AAT Tyr	GAT Asp	GGT Gly	ACT Thr	318					
40																45	50				
TTT Phe	AAA Lys	TAT Tyr	CAA Gln	TCT Ser	AGA Arg	CCA Pro	AAA Lys	TTT Phe	AAC Asn	TCA Ser	ACA Thr	CCT Pro	AAA Lys	TAT Tyr	ATT Ile	366					
55																60	65		70		
AAA Lys	TTC Phe	AAA Lys	CAT His	GAC Asp	TAT Tyr	AAT Asn	ATT Ile	TTA Leu	GAA Glu	TTT Phe	AAC Asn	GAT Asp	GGT Gly	ACA Thr	TTC Phe	414					
75																80	85				
GAA Glu	TAT Tyr	GGT Gly	GCA Ala	CGT Arg	CCA Pro	CAA Gln	TTT Phe	AAT Asn	AAA Lys	CCA Pro	GCA Ala	GCG Ala	AAA Lys	ACT Thr	GAT Asp	462					
90																95	100				
GCA Ala	ACT Thr	ATT Ile	AAA Lys	AAA Lys	GAA Glu	CAA Gln	AAA Lys	TTG Leu	ATT Ile	CAA Gln	GCT Ala	CAA Gln	AAT Asn	CTT Leu	GTG Val	510					
105																110	115				
AGA Arg	GAA Glu	TTT Phe	GAA Glu	AAA Lys	ACA Thr	CAT His	ACT Thr	GTC Val	AGT Ser	GCA Ala	CAC His	AGA Arg	AAA Lys	GCA Ala	CAA Gln	558					
120																125	130				
AAG Lys	GCA Ala	GTC Val	AAC Asn	TTA Leu	GTT Val	TCG Ser	TTT Phe	GAA Glu	TAC Tyr	AAA Lys	GTG Val	AAG Lys	AAA Lys	ATG Met	GTC Val	606					
135																140	145		150		
TTA Leu	CAA Gln	GAG Glu	CGA Arg	ATT Ile	GAT Asp	AAT Asn	GTA Val	TTA Leu	AAA Lys	CAA Gln	GGA Gly	TTA Leu	GTG Val	AGA Arg	TAA *	654					
155																160	165				
TACTTCTGTC ATTATTTTAA GTTCAAATA ATTTAATATT ATATTATTTT TTATTAATAA																714					
AACGACTATG CTATTTAATG CCAGGTTAAT GTAACTTTCC TAAAAATGAC TATATAATCG																774					
TTAAGTATCA ATTTTAAGGA GAGTTTACA ATG Met AAA Lys TTT Phe AAA Lys AAA Lys TAT Tyr ATA Ile TTA Leu																827					
1																5					
ACA Thr	GGA Gly	ACA Thr	TTA Leu	GCA Ala	TTA Leu	CTT Leu	TTA Leu	TCA Ser	TCA Ser	ACT Thr	GGG Gly	ATA Ile	GCA Ala	ACT Thr	ATA Ile	875					
10																15		20			
GAA Glu	GGG Gly	AAT Asn	AAA Lys	GCA Ala	GAT Asp	GCA Ala	AGT Ser	AGT Ser	CTG Leu	GAC Asp	AAA Lys	TAT Tyr	TTA Leu	ACT Thr	GAA Glu	923					
25																30		35		40	
AGT Ser	CAG Gln	TTT Phe	CAT His	GAT Asp	AAA Lys	CGC Arg	ATA Ile	GCA Ala	GAA Glu	GAA Glu	TTA Leu	AGA Arg	ACT Thr	TTA Leu	CTT Leu	971					
45																50		55			

AAC AAA TCG AAT GTA TAT GCA TTA GCT GCA GGA AGC TT 1009
Asn Lys Ser Asn Val Tyr Ala Leu Ala Ala Gly Ser
60 65

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 781 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATAGATAACT ATATTTTGTG TATATTATA AGTGTTTATA GTTAATTAAT AATTAGTTAA	60
TTTCAAAAGT TGTATAAATA GGATAACTTA ATAAATGTAA GATAATAATT TGGAGGATAA	120
TTAACATGAA AAATAAATTG ATAGCAAAAT CTTTATTAACT AATAGCGGCA ATTGGTATTA	180
CTACAACCTAC AATTGCGGTCA ACAGCAGATG CGAGCGAAGG ATACGGTCCA AGAGAAAAGA	240
AACCAAGTGAG TATTAATCAC AATATCGTAG AGTACAATGA TGGTACTTTT AAATATCAAT	300
CTAGACCAAA ATTTAACTCA ACACCTAAAT ATATTAAATT CAAACATGAC TATAATATTT	360
TAGAATTTAA CGATGGTACA TTCGAATATG GTGCACGTCC ACAATTTAAT AAACCAGCAG	420
CGAAAACCTGA TGCAACTATT AAAAAAGAAC AAAAATTGAT TCAAGCTCAA AATCTTGTGA	480
GAGAATTTGA AAAAACACAT ACTGTCAGTG CACACAGAAA AGCACAAAAG GCAGTCAACT	540
TAGTTTCGTT TGAATACAAA GTGAAGAAAA TGGTCTTACA AGAGCGAATT GATAATGTAT	600
TAAACAAGG ATTAGTGAGA TAATACTTCT GTCATTATTT TAAGTTCAAA ATAATTTAAT	660
ATTATATTAT TTTTATTAA TAAACGACT ATGCTATTTA ATGCCAGTT AATGTAACCT	720
TCCTAAAATT GACTATATAA TCGTTAAGTA TCAATTTTAA GGAGAGTTTA CAATGAAATT	780
T	781

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAGATAGCT ATATTCAGTC TATATTATAA AGTGTTTATA GTTAATTAAT AATTAGTTAA	60
TTTCAAAAGT TGTATAAATA GGATAACTTA ATAAATGTAA GATAATAATT TGGAGGATAA	120
TTGACATGAA AAATGCATTG ATAGCAAAAT CTTTATTAACT ATTAGCGGCA ATAGGTATTAA	180
CTACAACATC AATTGCGTCA ACAGCAGATG CGAGCGAAGG ATACGGTCCA AGAGAAAAAG	240
AACCAGTGAG TATTAATCAC AATATCGTAG AGTACAATGA TGGTACTTTT AAATATCAAT	300
CTAGACCAAA ATTTAACTCA ACACCTAAAT ATATTAAATT CAAACATGAC TATAATATTT	360
TAGAATTTAA CGATGGTGACA TTCGAATATG GTGCACGTCC ACAATTTAAT AAACCAGCAG	420
CGAAAACATG TGCAACTATT AAAAAAGAAC AAAAATTGAT TCAAGCTCAA AATCTTGTA	480
GAGAATTGTA AAAAACACAT ACTGTCAGTG CACACAGAAA AGCACAAGG GCAGTCAACT	540
TAGTTTCGTT TGAATACAAA GTGAAGAAAA TGGTCTTACA AGAGCGAATT GATAATGTAT	600
TAAAACAAGG ATTAGTTAAA TAAAACTTCA ATCGTTGCTG TTATCTGGAA ATAATTAATT	660
AAATGTTATG TTAATTTTTG TTAATGAAAA AAGTAATCTA TTTAATGACA GGTAAATGTA	720
ATTGTCCTGA AATTGACTAT ATACTCAGTA AGTATCAATT TTAAGGAGAG CTTATAATGA	780
AATTT	785

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Lys	Asn	Lys	Leu	Ile	Ala	Lys	Ser	Leu	Leu	Thr	Ile	Ala	Ala	Ile
1			5						10					15	
Gly	Ile	Thr	Thr	Thr	Thr	Ile	Ala	Ser	Thr	Ala	Asp	Ala	Ser	Glu	Gly
			20						25					30	
Tyr	Gly	Pro	Arg	Glu	Lys	Lys	Pro	Val	Ser	Ile	Asn	His	Asn	Ile	Val
			35					40						45	

Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn
50 55 60

Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu
65 70 75 80

Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys
85 90 95

Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile
100 105 110

Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser
115 120 125

Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr
130 135 140

Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys
145 150 155 160

Gln Gly Leu Val Arg
165

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Lys Asn Ala Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile
1 5 10 15

Gly Ile Thr Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly
20 25 30

Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val
35 40 45

Glu Tyr Asn Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn
50 55 60

Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu
65 70 75 80

Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys
85 90 95

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Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile
    100                      105                      110

Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser
    115                      120                      125

Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr
    130                      135                      140

Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys
    145                      150                      155                      160

Gln Gly Leu Val Lys
    165

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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Ser Glu Gly Tyr Gly Pro Arg Glu Lys Lys Pro Val Ser Ile Asn His
 1          5          10          15

Asn Ile Val Glu Tyr Asn Asp Gly Ser Phe Lys Tyr Gln Ser Arg Pro
 20          25          30

Lys Phe Asn Ser Thr Pro Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn
 35          40          45

Ile Leu Glu Phe Asn Asp Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln
 50          55          60

Phe Asn Lys Pro Ala Ala Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln
 65          70          75          80

Lys Leu Ile Gln Ala Gln Asn Leu Val Arg Glu Phe Glu Lys Thr His
 85          90          95

Thr Val Ser Ala His Arg Lys Ala Gln Lys Ala Val Asn Leu Val Ser
 100         105         110

Phe Glu Tyr Lys Val Lys Lys Met Val Leu Gln Glu Arg Ile Asp Asn
 115         120         125

Val Leu Lys Gln Gly Leu Val Arg
 130         135

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(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Ala Ser Gln Tyr Gly Pro Arg Pro Gln Phe Asn Lys Thr Pro Lys Tyr
 1             5             10             15

Val Lys Tyr Arg Asp Ala Gly Thr Gly Ile Arg Glu Tyr Asn Asp Gly
      20             25             30

Thr Phe Gly Tyr Glu Ala Arg Pro Arg Phe Asn Lys Pro Ser Glu Thr
      35             40             45

Asn Ala Tyr Asn Val Thr Thr His Ala Asn Gly Gln Val Ser Tyr Gly
 50             55             60

Ala Arg Pro Thr Tyr Lys Lys Pro Ser Glu Thr Asn Ala Tyr Asn Val
 65             70             75             80

Thr Thr His Ala Asn Gly Gln Val Ser Tyr Gly Ala Arg Pro Thr Gln
      85             90             95

Asn Lys Pro Ser Glu Thr Asn Ala Tyr Asn Val Thr Thr His Gly Asn
      100            105            110

Gly Gln Val Ser Tyr Gly Ala Arg Gln Ala Gln Asn Lys Pro Ser Lys
      115            120            125

Thr Asn Ala Tyr Asn Val Thr Thr His Ala Asn Gly Gln Val Ser Tyr
      130            135            140

Gly Ala Arg Pro Thr Tyr Lys Lys Pro Ser Lys Thr Asn Ala Tyr Asn
      145            150            155            160

Val Thr Thr His Ala Asp Gly Thr Ala Thr Tyr Gly Pro Arg Val Thr
      165            170            175

Lys
  
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